



2163

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RAW SEQUENCE LISTING

DATE: 02/28/2002

PATENT APPLICATION: US/09/910,071

TIME: 09:28:42

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02282002\I910071.raw

Similar

3 <110> APPLICANT: Tomikawa, Mayumi
 4 Aikawa, Seiichi
 5 Matsuzawa, Fumiko
 7 <120> TITLE OF INVENTION: Method and Apparatus for Extracting and Evaluating Mutually
 8 Portions in One-Dimensional Sequences in Molecules and/or Three-Dimensional
 9 Structures of Molecules
 11 <130> FILE REFERENCE: 522.1921D2
 13 <140> CURRENT APPLICATION NUMBER: 09/910,071
 14 <141> CURRENT FILING DATE: 2001-07-23
 16 <150> PRIOR APPLICATION NUMBER: US 08/014,867
 17 <151> PRIOR FILING DATE: 1993-02-08
 19 <160> NUMBER OF SEQ ID NOS: 20
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 37
 25 <212> TYPE: PRT
 26 <213> ORGANISM: human
 28 <400> SEQUENCE: 1
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 34 His Thr Val Glu Gly Gly Lys His Lys Thr Gly Pro Asn Leu His Gly
 35 20 25 30
 38 Leu Phe Gly Arg Lys
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 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 39
 44 <212> TYPE: PRT
 45 <213> ORGANISM: bacterium
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 49 Glu Gly Asp Asp Ala Ala Ala Gly Glu Lys Val Ser Lys Lys Cys Leu
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 61 <210> SEQ ID NO: 3
 62 <211> LENGTH: 51
 63 <212> TYPE: PRT
 64 <213> ORGANISM: rat
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 68 Met Ser Leu Ala Ile Leu Arg Val Ile Arg Leu Val Arg Val Phe Arg
 69 1 5 10 15
 72 Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu Gln Ile Leu Gly Arg

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81          50
84 <210> SEQ ID NO: 4
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87 <213> ORGANISM: unknown
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Figure 23A
92 <400> SEQUENCE: 4
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98 Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met
99          20          25          30
102 Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile
103          35          40          45
106 Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu Phe
107          50          55          60
110 Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Ser Glu Glu Glu Ile
111 65          70          75          80
114 Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser
115          85          90          95
118 Ala Ala Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr
119          100          105          110
122 Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala Asn Ile Asp Gly Asp
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127          130          135          140
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132 <212> TYPE: PRT
133 <213> ORGANISM: unknown
135 <220> FEATURE:
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145          20          25          30
148 Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly
149          35          40          45
152 Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp
153          50          55          60
156 Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu Val Met Val
157 65          70          75          80
160 Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala
161          85          90          95

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164 Asp Cys Phe Arg Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile
165           100           105           110
168 Glu Glu Leu Gly Glu Ile Leu Arg Ala Thr Gly Glu His Val Thr Glu
169           115           120           125
172 Glu Asp Ile Glu Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly
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183 <213> ORGANISM: unknown
185 <220> FEATURE:
186 <223> OTHER INFORMATION: calmodulin probe site 81-108, Figure 25, target
188 <400> SEQUENCE: 6
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199 <211> LENGTH: 28
200 <212> TYPE: PRT
201 <213> ORGANISM: unknown
203 <220> FEATURE:
204 <223> OTHER INFORMATION: calmodulin probe site 81-108, probe, Figure 25
206 <400> SEQUENCE: 7
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217 <211> LENGTH: 27
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219 <213> ORGANISM: unknown
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Calmodulin probe site 117-143, Figure 26, target
224 <400> SEQUENCE: 8
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235 <211> LENGTH: 27
236 <212> TYPE: PRT
237 <213> ORGANISM: unkown
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242 1           5           10           15
245 Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala

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Input Set : A:\PTO.VSK.txt

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255 <223> OTHER INFORMATION: Coordinates of C-alpha corresponding to the aminon acid
residue N
256      os. 7 to 14 in elongation factor of protein which is a binding si
257      te for phosphoric acid of GTP
259 <400> SEQUENCE: 10
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265 <210> SEQ ID NO: 11
266 <211> LENGTH: 8
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270 <220> FEATURE:
271 <223> OTHER INFORMATION: adenylate kinase - target
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281 <212> TYPE: PRT
282 <213> ORGANISM: unknown
284 <220> FEATURE:
285 <223> OTHER INFORMATION: ras protein - target
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295 <212> TYPE: PRT
296 <213> ORGANISM: unknown
298 <220> FEATURE:
299 <223> OTHER INFORMATION: adenylate kinase (3ADK)
301 <400> SEQUENCE: 13
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308 <211> LENGTH: 223
309 <212> TYPE: PRT
310 <213> ORGANISM: unknown
312 <220> FEATURE:
313 <223> OTHER INFORMATION: amino acid sequence of trypsin
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321 Ser Leu Asn Ser Gly Tyr His Phe Cys Gly Gly Ser Leu Ile Asn Ser

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322          20          25          30
325 Gln Trp Val Val Ser Ala Ala His Cys Tyr Lys Ser Gly Ile Gln Val
326          35          40          45
329 Arg Leu Gly Glu Asp Asn Ile Asn Val Val Glu Gly Asn Glu Gln Phe
330          50          55          60
333 Ile Ser Ala Ser Lys Ser Ile Val His Pro Ser Tyr Asn Ser Asn Thr
334 65          70          75          80
337 Leu Asn Asn Asp Ile Met Leu Ile Lys Leu Lys Ser Ala Ala Ser Leu
338          85          90          95
341 Asn Ser Arg Val Ala Ser Ile Ser Leu Pro Thr Ser Cys Ala Ser Ala
342          100          105          110
345 Gly Thr Gln Cys Leu Ile Ser Gly Trp Gly Asn Thr Lys Ser Ser Gly
346          115          120          125
349 Thr Ser Tyr Pro Asp Val Leu Lys Cys Leu Lys Ala Pro Ile Leu Ser
350          130          135          140
353 Asp Ser Ser Cys Lys Ser Ala Tyr Pro Gly Gln Ile Thr Ser Asn Met
354 145          150          155          160
357 Phe Cys Ala Gly Tyr Leu Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp
358          165          170          175
361 Ser Gly Gly Pro Val Val Cys Ser Gly Lys Leu Gln Gly Ile Val Ser
362          180          185          190
365 Trp Gly Ser Gly Cys Ala Gln Lys Asn Lys Pro Gly Val Tyr Thr Lys
366          195          200          205
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374 <211> LENGTH: 239
375 <212> TYPE: PRT
376 <213> ORGANISM: unknown
378 <220> FEATURE:
379 <223> OTHER INFORMATION: amino acid sequence of Elastase
381 <400> SEQUENCE: 15
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388          20          25          30
391 Thr Leu Ile Arg Gln Asn Trp Val Met Thr Ala Ala His Cys Val Asp
392          35          40          45
395 Arg Glu Leu Thr Phe Arg Val Val Val Gly Glu His Asn Leu Asn Gln
396          50          55          60
399 Asn Asn Gly Thr Glu Gln Tyr Val Gly Val Gln Lys Ile Val Val Pro
400 65          70          75          80
403 Tyr Trp Asn Thr Asp Asp Val Ala Ala Gly Tyr Asp Ile Ala Leu Leu
404          85          90          95
407 Arg Leu Ala Gln Ser Val Thr Leu Asn Ser Tyr Val Gln Leu Gly Val
408          100          105          110
411 Leu Pro Arg Ala Gly Thr Ile Leu Ala Asn Ser Pro Cys Tyr Ile Thr
412          115          120          125
415 Thr Gly Trp Gly Leu Thr Arg Thr Asn Gly Gln Leu Ala Gln Thr Leu

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VERIFICATION SUMMARY

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